

# SEQUENCE LISTING

<110> Mathur, Brian  
Turner, C. Alexander Jr.

<120> Novel Human Lipocalin Homologs and Polynucleotides Encoding the Same

<130> LEX-0173-USA

<150> US 60/203,874

<151> 2000-05-12

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<213> homo sapiens

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<213> homo sapiens

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			20					25					30		
Phe	Ser	Gly	Leu	Trp	Tyr	Val	Val	Ser	Met	Ala	Ser	Asp	Cys	Arg	Val
		35				40					45				
Phe	Leu	Gly	Lys	Lys	Asp	His	Leu	Ser	Met	Ser	Thr	Arg	Ala	Ile	Arg
	50					55				60					
Pro	Thr	Glu	Glu	Gly	Gly	Leu	His	Val	His	Met	Glu	Phe	Pro	Gly	Ala
65				70					75					80	
Asp	Gly	Cys	Asn	Gln	Val	Asp	Ala	Glu	Tyr	Leu	Lys	Val	Gly	Ser	Glu
			85					90					95		
Gly	His	Phe	Arg	Val	Pro	Ala	Leu	Gly	Tyr	Leu	Asp	Val	Arg	Ile	Val
		100					105					110			
Asp	Thr	Asp	Tyr	Ser	Ser	Phe	Ala	Val	Leu	Tyr	Ile	Tyr	Lys	Glu	Leu
	115						120					125			

Glu Gly Ala Leu Ser Thr Met Val Gln Leu Tyr Ser Arg Thr Gln Asp  
 130 135 140  
 Val Ser Pro Gln Ala Leu Lys Ala Phe Gln Asp Phe Tyr Pro Thr Leu  
 145 150 155 160  
 Gly Leu Pro Glu Asp Met Met Val Met Leu Pro Gln Ser Asp Ala Cys  
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 gaggttctgc tgcagcctga cttcaatgct gaaaagggtc ttctgggca agaaggacca 120  
 cctgtccatg tccaccaggg ccatcaggcc cacagaggag gggggcctcc acgtccacat 180  
 ggagttcccc ggggaggac gctgtaa 207

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 20 25 30  
 Gly Leu Pro Gly Gln Glu Gly Pro Pro Val His Val His Gln Gly His  
 35 40 45  
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 tccatggcat ctgactgcag ggtcttctct ggcaagaagg accacctgtc catgtccacc 180  
 agggccatca ggccacaga ggaggggggc ctccacgtcc acatggagtt cccgggggag 240  
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<400> 6

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20 25 30  
Phe Ser Gly Leu Trp Tyr Val Val Ser Met Ala Ser Asp Cys Arg Val  
35 40 45  
Phe Leu Gly Lys Lys Asp His Leu Ser Met Ser Thr Arg Ala Ile Arg  
50 55 60  
Pro Thr Glu Glu Gly Gly Leu His Val His Met Glu Phe Pro Gly Ala  
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Pro Pro Pro Ala Cys Gly Met Pro Cys Gly Thr Ser Leu Ser Ile Gln  
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ttctcaggcc tctggtagct ggtctccatg gcatctgact gcagggtctt cctgggcaag 180  
aaggaccacc tgtccatgtc caccagggcc atcaggccca cagaggaggg cggcctccac 240  
gtccacatgg agttcccggg ggcggacggc tgtaaccagg tggatgccga gtacctgaag 300  
gtgggctccg agggacactt cagagtcctt gccttgggct acctggacgt gcgcatcgtg 360  
gacacagact acagctcctt cgccgtcctt tacatctaca aggagctgga ggggagcgtc 420  
agcaccatgg tgcagctcta cagccggacc caggatgtga gtccccaggc tctgaaggcc 480  
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 Gln Pro Asp Phe Asn Ala Glu Lys Phe Ser Gly Leu Trp Tyr Val Val  
 35 40 45  
 Ser Met Ala Ser Asp Cys Arg Val Phe Leu Gly Lys Lys Asp His Leu  
 50 55 60  
 Ser Met Ser Thr Arg Ala Ile Arg Pro Thr Glu Glu Gly Gly Leu His  
 65 70 75 80  
 Val His Met Glu Phe Pro Gly Ala Asp Gly Cys Asn Gln Val Asp Ala  
 85 90 95  
 Glu Tyr Leu Lys Val Gly Ser Glu Gly His Phe Arg Val Pro Ala Leu  
 100 105 110  
 Gly Tyr Leu Asp Val Arg Ile Val Asp Thr Asp Tyr Ser Ser Phe Ala  
 115 120 125  
 Val Leu Tyr Ile Tyr Lys Glu Leu Glu Gly Ala Leu Ser Thr Met Val  
 130 135 140  
 Gln Leu Tyr Ser Arg Thr Gln Asp Val Ser Pro Gln Ala Leu Lys Ala  
 145 150 155 160  
 Phe Gln Asp Phe Tyr Pro Thr Leu Gly Leu Pro Glu Asp Met Met Val  
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 ggtcttcttg ggcaagaagg accacctgtc catgtccacc agggccatca ggcccacaga 180  
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 20 25 30  
 Gln Pro Asp Phe Asn Ala Glu Lys Gly Leu Pro Gly Gln Glu Gly Pro  
 35 40 45  
 Pro Val His Val His Gln Gly His Gln Ala His Arg Gly Gly Arg Pro  
 50 55 60

Pro Arg Pro His Gly Val Pro Gly Gly Gly Arg Leu  
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<210> 13  
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ttctcaggcc tctggtagct ggtctccatg gcattctgact gcagggtctt cctgggcaag 180  
aaggaccacc tgtccatgtc caccagggcc atcaggccca cagaggaggc cggcctccac 240  
gtccacatgg agttcccggg ggcggacggc tgtaaccagg tggatgccga gtacctggag 300  
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<210> 14  
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<212> PRT  
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<400> 14  
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20 25 30  
Gln Pro Asp Phe Asn Ala Glu Lys Phe Ser Gly Leu Trp Tyr Val Val  
35 40 45  
Ser Met Ala Ser Asp Cys Arg Val Phe Leu Gly Lys Lys Asp His Leu  
50 55 60  
Ser Met Ser Thr Arg Ala Ile Arg Pro Thr Glu Gly Gly Leu His  
65 70 75 80  
Val His Met Glu Phe Pro Gly Ala Asp Gly Cys Asn Gln Val Asp Ala  
85 90 95  
Glu Tyr Leu Glu Ser Leu His Pro Pro Pro Pro Ala Cys Gly Met Pro  
100 105 110  
Cys Gly Thr Ser Leu Ser Ile Gln  
115 120

<210> 15  
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gtaccagggg cctctgctgt cctgtggtgg gtgggagctg ggcccctgcc agagacaacg 180  
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<210> 16  
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<212> PRT  
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<400> 16

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          20           25           30
Gln Pro Asp Phe Asn Ala Glu Lys Val Pro Gly Ala Ser Ala Val Leu
          35           40           45
Trp Trp Val Gly Ala Gly Pro Leu Pro Glu Thr Thr
          50           55           60
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<210> 17

<211> 597

<212> DNA

<213> homo sapiens

<400> 17

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gacttcaatg ctgaaaagtt ctcaggcctc tggtagctgg tctccatggc atctgactgc      180
agggtcttcc tgggcaagaa ggaccacctg tccatgtcca ccagggccat caggcccaca      240
gaggagggcg gcctccacgt ccacatggag ttcccggggg cggacggctg taaccagggtg      300
gatgccagat acctgaaggt gggctccgag ggacacttca gagtcccggc cttgggctac      360
ctggacgtgc gcacgtgga cacagactac agctccttcg ccgtccttta catctacaag      420
gagctggagg gggcgctcag caccatgggtg cagctctaca gccggaccca ggatgtgagt      480
ccccaggctc tgaaggcctt ccaggacttc taccgaccc tggggctccc cgaggacatg      540
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<210> 18

<211> 198

<212> PRT

<213> homo sapiens

<400> 18

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          20           25           30
Gln Ala Glu Val Leu Leu Gln Pro Asp Phe Asn Ala Glu Lys Phe Ser
          35           40           45
Gly Leu Trp Tyr Val Val Ser Met Ala Ser Asp Cys Arg Val Phe Leu
          50           55           60
Gly Lys Lys Asp His Leu Ser Met Ser Thr Arg Ala Ile Arg Pro Thr
          65           70           75           80
Glu Glu Gly Gly Leu His Val His Met Glu Phe Pro Gly Ala Asp Gly
          85           90           95
Cys Asn Gln Val Asp Ala Glu Tyr Leu Lys Val Gly Ser Glu Gly His
          100          105          110
Phe Arg Val Pro Ala Leu Gly Tyr Leu Asp Val Arg Ile Val Asp Thr
          115          120          125
Asp Tyr Ser Ser Phe Ala Val Leu Tyr Ile Tyr Lys Glu Leu Glu Gly
          130          135          140
Ala Leu Ser Thr Met Val Gln Leu Tyr Ser Arg Thr Gln Asp Val Ser
          145          150          155          160
Pro Gln Ala Leu Lys Ala Phe Gln Asp Phe Tyr Pro Thr Leu Gly Leu
          165          170          175
Pro Glu Asp Met Met Val Met Leu Pro Gln Ser Asp Ala Cys Asn Pro
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Glu Ser Lys Glu Ala Pro  
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185

190

<210> 19  
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<212> DNA  
<213> homo sapiens

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gacttcaatg ctgaaaaggg tcttcctggg caagaaggac cacctgtcca tgtccaccag 180  
ggccatcagg cccacagagg agggcggcct ccacgtccac atggagttcc cgggggcgga 240  
cggctgttaa 249

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<211> 82  
<212> PRT  
<213> homo sapiens

<400> 20  
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20 25 30  
Gln Ala Glu Val Leu Leu Gln Pro Asp Phe Asn Ala Glu Lys Gly Leu  
35 40 45  
Pro Gly Gln Glu Gly Pro Pro Val His Val His Gln Gly His Gln Ala  
50 55 60  
His Arg Gly Gly Arg Pro Pro Arg Pro His Gly Val Pro Gly Gly Gly  
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Arg Leu

<210> 21  
<211> 381  
<212> DNA  
<213> homo sapiens

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gacttcaatg ctgaaaagtt ctcaggcctc tggtagctgg tctccatggc atctgactgc 180  
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<213> homo sapiens

<400> 22  
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20           25           30
Gln Ala Glu Val Leu Leu Gln Pro Asp Phe Asn Ala Glu Lys Phe Ser
35           40           45
Gly Leu Trp Tyr Val Val Ser Met Ala Ser Asp Cys Arg Val Phe Leu
50           55           60
Gly Lys Lys Asp His Leu Ser Met Ser Thr Arg Ala Ile Arg Pro Thr
65           70           75           80
Glu Glu Gly Gly Leu His Val His Met Glu Phe Pro Gly Ala Asp Gly
85           90           95
Cys Asn Gln Val Asp Ala Glu Tyr Leu Glu Ser Leu His Pro Pro
100          105          110
Pro Ala Cys Gly Met Pro Cys Gly Thr Ser Leu Ser Ile Gln
115          120          125

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<210> 23  
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gacttcaatg ctgaaaaggt accaggggcc tctgctgtcc tgtggtgggt gggagctggg      180
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20           25           30
Gln Ala Glu Val Leu Leu Gln Pro Asp Phe Asn Ala Glu Lys Val Pro
35           40           45
Gly Ala Ser Ala Val Leu Trp Trp Val Gly Ala Gly Pro Leu Pro Glu
50           55           60
Thr Thr
65

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<210> 25  
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 <213> homo sapiens

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ggctgtaacc aggtggatgc cgagtacctg aaggtgggct ccgagggaca cttcagagtc      180
ccggccttgg gctacctgga cgtgcgcatac gtggacacag actacagctc cttcgccgtc      240
ctttacatct acaaggagct ggagggggcg ctcagcacca tgggtgcagct ctacagccgg      300
accaggatg tgagtcccca ggctctgaag gccttccagg acttctaccc gaccctgggg      360

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<400> 26  
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20 25 30  
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35 40 45  
Tyr Leu Lys Val Gly Ser Glu Gly His Phe Arg Val Pro Ala Leu Gly  
50 55 60  
Tyr Leu Asp Val Arg Ile Val Asp Thr Asp Tyr Ser Ser Phe Ala Val  
65 70 75 80  
Leu Tyr Ile Tyr Lys Glu Leu Glu Gly Ala Leu Ser Thr Met Val Gln  
85 90 95  
Leu Tyr Ser Arg Thr Gln Asp Val Ser Pro Gln Ala Leu Lys Ala Phe  
100 105 110  
Gln Asp Phe Tyr Pro Thr Leu Gly Leu Pro Glu Asp Met Met Val Met  
115 120 125  
Leu Pro Gln Ser Asp Ala Cys Asn Pro Glu Ser Lys Glu Ala Pro  
130 135 140

<210> 27  
<211> 216  
<212> DNA  
<213> homo sapiens

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ggctgtaacc aggtggatgc cgagtacctg gagtctctcc atcctccacc ccccgctgt 180  
gggatgcctt gtgggacgtc tctttctatt caataa 216

<210> 28  
<211> 71  
<212> PRT  
<213> homo sapiens

<400> 28  
Met Ala Ser Asp Cys Arg Val Phe Leu Gly Lys Lys Asp His Leu Ser  
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20 25 30  
His Met Glu Phe Pro Gly Ala Asp Gly Cys Asn Gln Val Asp Ala Glu  
35 40 45  
Tyr Leu Glu Ser Leu His Pro Pro Pro Pro Ala Cys Gly Met Pro Cys  
50 55 60  
Gly Thr Ser Leu Ser Ile Gln  
65 70